Fig. 1.

CTCATGAGAAGGAGAAGTGCGTCAGCATTTTCTAGACTGTCATTTCTACTTTAGCTGAGT
TGCTGGGAATGAAATCTTCTCTTGTACCCCTGCCTGGTTGCTGGAATAAAAATGTTTAAT
TTGGATTGTTAACCTGTTTTCCAGAGTTACCGGACTCAAAATTGAGCTACTGGGGGAAAC
TTCTATTGCATCAACCATATCATACCTAGAC**A/T***ATGCTTTTTGTCTTCATTGGCTCAAG*
CTACGGAGATTCACAGGTACTTTTAACTGTTGAGTGCATCTTGGTGCAATAAGTTGGTTT
TTAGAGCTGCCTTATTGTATTTTCCATACAGTAGCCTTTCATTCATTTGGAACATTGAGG
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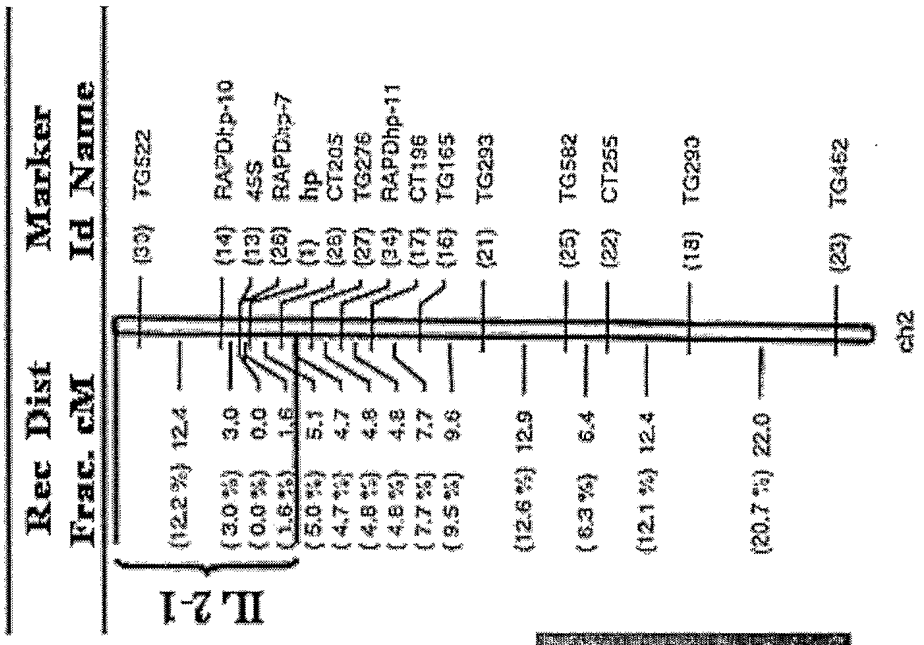
TTTGAATTCACGTTTAGCTTGTAAAGCTCAATCTCCAGCCTGACACCAAA


Marker Id Name
Rec Dist
Frac. cM
IL 2-1
(30) TG522
(14) RAPDhp-10
(13) 45S
(26) RAPDhp-7
(1) hp
(28) CT205
(27) TG276
(34) RAPDhp-11
(17) CT196
(16) TG165
(21) TG293
(25) TG582
(22) CT255
(18) TG290
(23) TG452
(12.2 %) 12.4
(3.0 %) 3.0
(0.0 %) 0.0
(1.6 %) 1.6
(5.0 %) 5.1
(4.7 %) 4.7
(4.8 %) 4.8
(4.8 %) 4.8
(7.7 %) 7.7
(9.5 %) 9.6
(12.6 %) 12.9
(6.3 %) 6.4
(12.1 %) 12.4
(20.7 %) 22.0
ch2

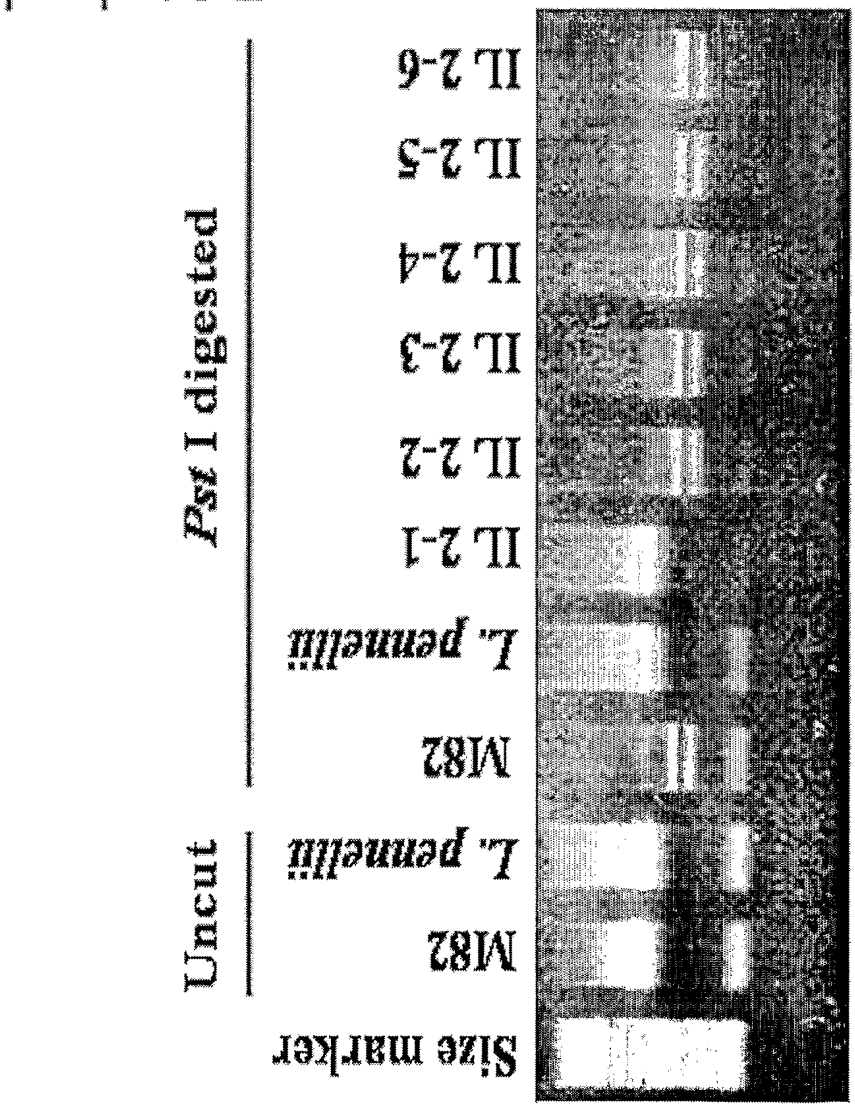
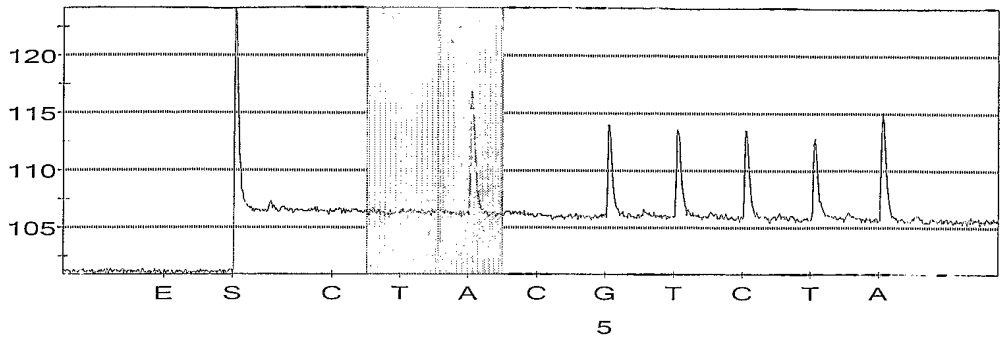

Size marker
M82
L. pennellii
M82
L. pennellii
IL 2-1
IL 2-2
IL 2-3
IL 2-4
IL 2-5
IL 2-6
Uncut
Pst I digested

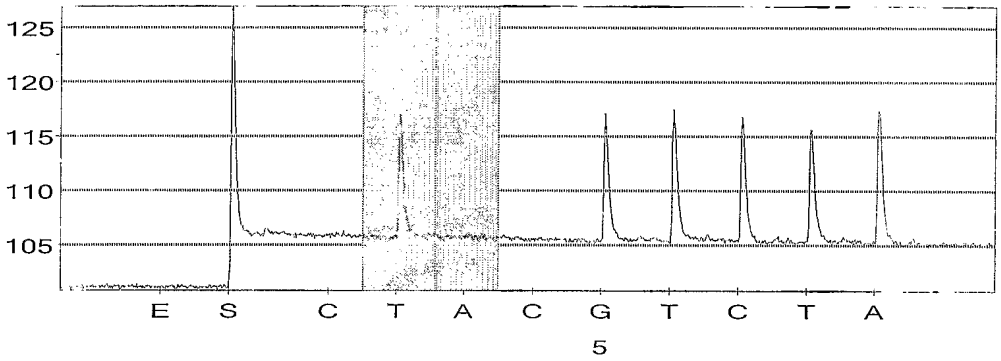
Fig. 2

Fig. 3

a. *hp-1/hp-1*



b. +/+



c. *hp-1/+*

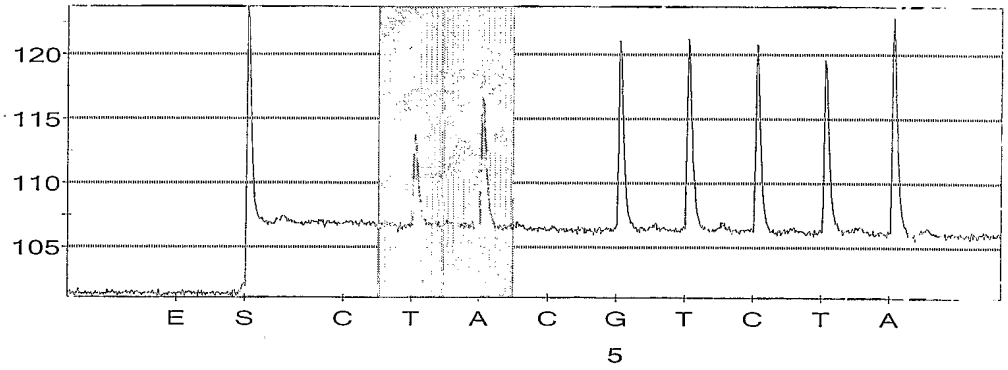


Fig. 4

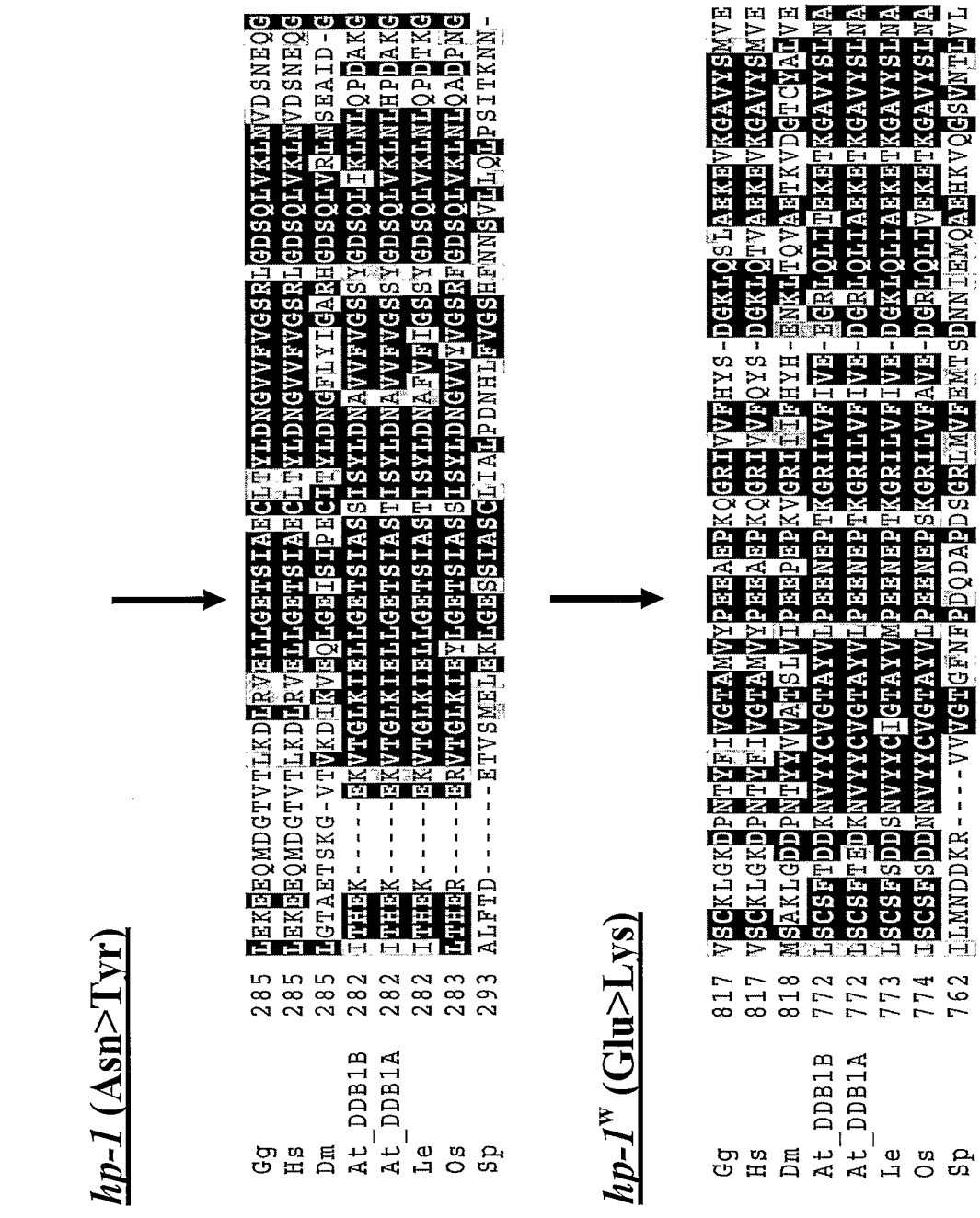

a.
hp-1 (Asn>Tyr)
Gg 285
Hs 285
Dm 285
At_DDB1B 282
At_DDB1A 282
Le 282
Os 283
Sp 293
b.
hp-1w (Glu>Lys)
Gg 817
Hs 817
Dm 818
At_DDB1B 772
At_DDB1A 772
Le 773
Os 774
Sp 762

Fig. 5

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   1 ATGAGTGTATGGAACTACGTGGTTACGGCTCACAAACCAACAAATGTTACACATTCCTGTGTTGGCAATTTCACCGGTCC
  81 TCAAGAGCTCAATCTTATCATTGCGAAATGTACTCGAATCGAGATTCATTTACTTACTCCCCAAGGTTTACAGCCTATGT
 161 TAGATGTGCCAATATATGGGAGGATCGCGACACTTGAGCTTTTTCGTCCTCACGGTGAAACACAAGATCTTCTCTTCATC
 241 GCAACAGAGCGATATAAATTCTGTGTCCTTCAATGGGATACTGAGGCATCTGAAGTTATCACAAGAGCAATGGGAGATGT
 321 GTCAGACCGAATAGGCCGTCCCACAGATAATGGTCAGATTGGTATAATTGATCCAGATTGCAGATTGATCGGGCTACATC
 401 TTTATGATGGACTATTTAAGGTTATTCCATTTGATAACAAAGGCCAACTGAAGGAAGCTTTTAACATCAGGCTCGAGGAG
 481 CTTCAAGTTTTAGATATTAAATTCTTGTATGGTTGCCCAAAGCCTACAATTGTTGTTCTATATCAGGATAACAAGGATGC
 561 CCGGCATGTCAAAACATATGAGGTGTCCTTGAAAGACAAAGATTTTATTGAAGGGCCATGGGCTCAAAATAATCTTGATA
 641 ATGGAGCTTCTTTGCTAATACCAGTACCTCCACCACTGTGTGGTGTATTGATTATTGGAGAAGAAACCATCGTTTATTGC
 721 AGCGCTTCAGCTTTTAAGGCTATCCCAATTAGACCTTCTATCACAAGAGCATATGGGCGGGTTGATGCTGATGGTTCTCG
 801 ATATTTGCTTGGGGATCATAATGGGCTTCTTCACCTACTTGTAATCACTCATGAGAAGGAGAAAGTTACCGGACTCAAAA
 881 TTGAGCTACTGGGGGAAACTTCTATTGCATCAACCATATCATACCTAGACAATGCTTTTGTCTTCATTGGCTCAAGCTAC
 961 GGAGATTCACAGCTTGTAAAGCTCAATCTCCAGCCTGACACCAAAGGTTCTTATGTGGAAGTTCTAGAGAGATATGTCAA
1041 TTTAGGACCTATTGTGGACTTCTGTGTTGTTGATCTGGAAAGGCAAGGTCAAGGTCAGGTTGTAACTTGCTCTGGAGCCT
1121 ATAAGGATGGATCACTTCGTATTGTTCGAAATGGAATTGGCATAAATGAACAGGCGTCTGTGGAACTACAAGGGATCAAA
1201 GGAATGTGGTCTCTTAGATCTGCTACTGATGATCCATATGACACATTCTTGGTTGTTAGCTTCATTAGTGAGACACGCGT
1281 TTTGGCTATGAACCTTGAGGATGAGCTGGAAGAAACTGAGATAGAAGGCTTCAATTCTCAAGTCCAGACCTTGTTTTGTC
1361 ATGATGCTGTATACAACCAGCTTGTTCAGGTTACTTCAAATTCTGTTAGATTGGTCAGTTCTACCTCTAGAGATCTGAAA
1441 AACGAGTGGTTTGCCCCAGTCGGCTACTCGGTCAATGTTGCAACTGCTAATGCCACTCAGGTACTATTGGCTACTGGGGG
1521 TGGCCATCTGGTATACCTAGAAATTGGTGATGGGGTGTTGAATGAAGTAAAATATGCCAAGTTGGATTATGATATCTCGT
1601 GCCTGGACATAAATCCAATTGGTGAAAATCCGAACTACAGTAACATTGCAGCAGTTGGAATGTGGACAGACATAAGTGTC
1681 AGGATATATTCACTTCCTGACTTGAATCTCATTACAAAGGAACAGCTAGGAGGGGAGATAATTCCTCGTTCTGTTCTGAT
1761 GTGTTCCTTCGAAGGGATATCTTATCTACTATGTGCTTTGGGAGATGGCCATCTCTTGAATTTTGTATTGAGCATGAGTA
1841 CTGGTGAGCTGACAGATAGGAAAAAAGTTTCTCTTGGGACACAGCCCATAACACTTCGTACATTCTCATCTAAAGATACT
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1921 ACACATGTCTTTGCTGCCTCCGATAGGCCAACAGTTATTTACAGCAGTAACAAGAAGCTGCTTTATAGCAATGTAAATCT

2001 AAAAGAAGTTAGTCATATGTGCCCATTCAATGTTGCAGCTTTTCCAGACAGCCTTGCAATCGCTAAAGAAGGTGAGTTAA

2081 CAATTGGCACTATTGATGAAATTCAAAAGCTTCACATTCGTTCAATACCCCTTGGGGAGCATGCACGTCGCATCAGCCAT

2161 CAAGAGCAGACCCGGACATTTGCTCTATGCAGTGTGAAGTATACTCAGTCAAATGCAGATGATCCTGAAATGCATTTTGT

2241 CCGCCTGTTGGATGATCAGACATTTGAGTTCATATCAACATATCCCCTTGACCAATTTGAATATGGCTGTTCCATACTAA

2321 GCTGCTCCTTTTCTGATGATAGTAATGTGTATTATTGCATTGGAACTGCATATGTGATGCCAGAGGAAAATG**G**AACCTACT

2401 AAGGGCCGAATTTTAGTTTTTATAGTTGAAGATGGAAAGCTCCAGCTAATTGCTGAGAAGGAAACTAAGGGAGCTGTCTA

2481 CTCTCTAAATGCCTTCAATGGGAAACTGCTTGCTGCAATCAATCAGAAGATTCAATTGTACAAGTGGGCTTCGCGTGAGG

2561 ATGGTGGCCAGCCGAGAATTGCAGACAGAATGTGGACACCATGGTCATATATTAGCTCTCTTTATGTTCAAACACGTGGGGAT

2641 TTCATTGTTGTTGGTGATTTGATGAAATCCATTTCTCTGCTGATTTTCAAGCATGAAGAGGGTGCTATAGAGGAGCGAGC

2721 CAGAGACTATAATGCAAATTGGATGTCAGCTGTTGAGATTCTCGATGATGACATTTATCTTGGTGCTGAGAATAACTTCA

2801 ACCTTTTCACGGTCAGGAAAAATAGTGAAGGTGCTACAGATGAGGAGCGCAGCCGTCTTGAAGTGGTTGGTGAATACCAC

2881 CTTGGCGAATTTGTTAATAGGTTTAGACATGGTTCACTTGTCATGCCGACTACCAGATTCAGATGTTGGGCAGATACCCAC

2961 TGTCATATTTGGCACAGTGAATGGTGTTATAGGGGTGATTGCATCACTACCTCATGATCAATATTATTTTTGGAGAAGC

3041 TGCAGACAAACTTACGGAAAGTGATAAAGGGTGTGGGAGGTCTGAGCCATGAGCAGTGGAGGTCGTTTTACAATGAGAAG

3121 AAAACAGTAGATGCTAAAAACTTTCTTGATGGAGATTTGATTGAATCATTCCTAGATCTTAGCAGGAATAGGATGGAAGA

3201 GATTTCAAAGGCTATGTCAGTTCCAGTTGAGGAACTAATGAAGAGAGTGGAAGAGTTGACAAGGTTGCATTAG

Fig. 6

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   1 MSVWNYVVTAHKPTNVTHSCVGNFTGPQELNLIIAKCTRIEIHLLTPQGLQPMLDVPIYGRIATLELFRPHGETQDLLFI
  81 ATERYKFCVLQWDTEASEVITRAMGDVSDRIGRPTDNGQIGIIDPDCRLIGLHLYDGLFKVIPFDNKGQLKEAFNIRLEE
 161 LQVLDIKFLYGCPKPTIVVLYQDNKDARHVKTYEVSLKDKDFIEGPWAQNNLDNGASLLIPVPPPLCGVLIIGEETIVYC
 241 SASAFKAIPIRPSITRAYGRVDADGSRYLLGDHNGLLHLLVITHEKEKVTGLKIELLGETSIASTISYLDNAFVFIGSSY
 321 GDSQLVKLNLQPDTKGSYVEVLERYVNLGPIVDFCVVDLERQGQGQVVTCSGAYKDGSLRIVRNGIGINEQASVELQGIK
 401 GMWSLRSATDDPYDTFLVVSFISETRVLAMNLEDELEETEIEGFNSQVQTLFCHDAVYNQLVQVTSNSVRLVSSTSRDLK
 481 NEWFAPVGYSVNVATANATQVLLATGGGHLVYLEIGDGVLNEVKYAKLDYDISCLDINPIGENPNYSNIAAVGMWTDISV
 561 RIYSLPDLNLTTKEQLGGEIIPRSVLMCSFEGISYLLLCALGDGHLLNFVLSMSTGELTDRKKVSLGTQPITLRTFSSKDT
 641 THVFAASDRPTVIYSSNKKLLYSNVNLKEVSHMCPFNVAAFPDSLATAKEGELTIGTIDEIQKLHIRSIPLGEHARRISH
 721 QEQTRTFALCSVKYTQSNADDPEMHFVRLLDDQTFEFISTYPLDQFEYGCSILSCSFSDDSNVYYCIGTAYVMPEENEPT
 801 KGRILVFIVEDGKLQLIAEKETKGAVYSLNAFNGKLLAAINQKIQLYKWASREDGGSRELQTECGHHGHILALYVQTRGD
 881 FIVVGDLMKSISLLIFKHEEGAIEERARDYNANWMSAVEILDDDIYLGAENNFNLFTVRKNSEGATDEERSRLEVVGEYH
 961 LGEFVNRFRHGSLVMRLPDSDVGQIPTVIFGTVNGVIGVIASLPHDQYLFLEKLQTNLRKVIKGVGGLSHEQWRSFYNEK
1041 KTVDAKNFLDGDLIESFLDLSRNRMEEISKAMSVPVEELMKRVEELTRLH
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